

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

## (ii) TITLE OF INVENTION:

## (iii) NUMBER OF SEQUENCES: 19

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Foley, Hoag & Eliot LLP  
(B) STREET: One Post Office Square  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: US  
(F) ZIP: 02109

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P.  
(B) REGISTRATION NUMBER: 36,709  
(C) REFERENCE/DOCKET NUMBER: SUV003.04

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-832-1000  
(B) TELEFAX: 617-832-7000

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 736 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AACNNCNTN NATGGCACCC CCNCCCAACC TTTNNNCCNN NTAANCAAAA NNCCCCNTTT 60  
NATACCCCT NTAANANTTT TCCACNNNC NNAAANNCCN CTGNANACNA NGNAAANCCN 120  
TTTTTNAACC CCCCCACCC GGAATTCNA NTNNCCNCCC CCAAATTACA ACTCCAGNCC 180

AAAATTNANA NAATTGGTCC TAACCTAACC NATNGTTGTT ACGGTTTCCC CCCCCAAATA 240  
 CATGCACTGG CCCGAACACT TGATCGTTGC CGTTCCAATA AGAATAAATC TGGTCATATT 300  
 AAACAAGCCN AAAGCTTTAC AAAGTGTGT ACAATTAATG GGCGAACACG AACTGTTCTGA 360  
 ATTCTGGTCT GGACATTACA AAGTGCACCA CATCGGATGG AACCAGGAGA AGGCCACAAC 420  
 CGTACTGAAC GCCTGGCAGA AGAAGTTCGC ACAGGTTGGT GGTGGCGCA AGGAGTAGAG 480  
 TGAATGGTGG TAATTTTTGG TTGTTCCAGG AGGTGGATCG TCTGACGAAG AGCAAGAAGT 540  
 CGTCGAATTA CATCTTCGTG ACGTTCTCCA CCGCCAATTT GAACAAGATG TTGAAGGAGG 600  
 CGTCGAANAC GGACGTGGTG AAGCTGGGGG TGGTGCTGGG GGTGGCGGCG GTGTACGGGT 660  
 GGGTGGCCCA GTCGGGGCTG GCTGCCTTGG GAGTGCTGGT CTTNGCGNGC TNCNATTCGC 720  
 CCTATAGTNA GNCGTA 736

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa	Pro	Pro	Pro	Asn	Tyr	Asn	Ser	Xaa	Pro	Lys	Xaa	Xaa	Xaa	Leu	Val	1	5	10	15
Leu	Thr	Pro	Xaa	Val	Val	Thr	Val	Ser	Pro	Pro	Lys	Tyr	Met	His	Trp	20	25	30	
Pro	Glu	His	Leu	Ile	Val	Ala	Val	Pro	Ile	Arg	Ile	Asn	Leu	Val	Ile	35	40	45	
Leu	Asn	Lys	Pro	Lys	Ala	Leu	Gln	Thr	Val	Val	Gln	Leu	Met	Gly	Glu	50	55	60	
His	Glu	Leu	Phe	Glu	Phe	Trp	Ser	Gly	His	Tyr	Lys	Val	His	His	Ile	65	70	75	80
Gly	Trp	Asn	Gln	Glu	Lys	Ala	Thr	Thr	Val	Leu	Asn	Ala	Trp	Gln	Lys	85	90	95	
Lys	Phe	Ala	Gln	Val	Gly	Gly	Trp	Arg	Lys	Glu	100	105							

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5187 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGTCTGTCA CCCGGAGCCG GAGTCCCCGG CGGCCAGCAG CGTCCTCGCG AGCCGAGCGC 60  
 CCAGGCGCGC CCGGAGCCCG CGGCGGCGGC GGCAACATGG CCTCGGCTGG TAACGCCGCC 120  
 GGGGCCCTGG GCAGGCAGGC CGGCGGCGGG AGGCGCAGAC GGACCGGGGG ACCGCACCGC 180  
 GCCGCGCCGG ACCGGGACTA TCTGCACCGG CCCAGCTACT GCGACGCCGC CTTGCTCTG 240  
 GAGCAGATTT CCAAGGGGAA GGCTACTGGC CGGAAAGCGC CGCTGTGGCT GAGAGCGAAG 300  
 TTTCAGAGAC TCTTATTTAA ACTGGGTTGT TACATTCAA AGAACTGCGG CAAGTTTTTG 360  
 GTTGTGGGTC TCCTCATATT TGGGGCCTTC GCTGTGGGAT TAAAGGCAGC TAATCTCGAG 420  
 ACCAACGTGG AGGAGCTGTG GGTGGAAGTT GGTGGACGAG TGAGTCGAGA ATTAAATTAT 480  
 ACCCGTCAGA AGATAGGAGA AGAGGCTATG TTTAATCCTC AACTCATGAT ACAGACTCCA 540  
 AAAGAAGAAG GCGCTAATGT TCTGACCACA GAGGCTCTCC TGCAACACCT GGAATCAGCA 600  
 CTCCAGGCCA GTCGTGTGCA CGTCTACATG TATAACAGGC AATGGAAGTT GGAACATTTG 660  
 TGCTACAAAT CAGGGGAAC TATCACGGAG ACAGGTTACA TGGATCAGAT AATAGAATAC 720  
 CTTTACCCTT GCTTAATCAT TACACCTTTG GACTGCTTCT GGAAGGGGC AAAGCTACAG 780  
 TCCGGGACAG CATACTCCT AGGTAAGCCT CCTTTACGGT GGACAACTT TGACCCCTTG 840  
 GAATTCCTAG AAGAGTTAAA GAAAATAAAC TACCAAGTGG ACAGCTGGGA GGAAATGCTG 900  
 AATAAGCCG AAGTTGGCCA TGGGTACATG GACCGGCCTT GCCTCAACCC AGCCGACCCA 960  
 GATTGCCCTG CCACAGCCCC TAACAAAAAT TCAACCAAAC CTCTTGATGT GGCCCTTGTT 1020  
 TTGAATGGTG GATGTCAAGG TTTATCCAGG AAGTATATGC ATTGGCAGGA GGAGTTGATT 1080  
 GTGGGTGGTA CCGTCAAGAA TGCCACTGGA AACTTTGTCA GCGCTCACGC CCTGCAACC 1140  
 ATGTTCCAGT TAATGACTCC CAAGCAAATG TATGAACACT TCAGGGGCTA CGACTATGTC 1200  
 TCTCACATCA ACTGGAATGA AGACAGGGCA GCCGCCATCC TGGAGGCCTG GCAGAGGACT 1260  
 TACGTGGAGG TGTTTCATCA AAGTGTGCGC CCAAACCTCA CTCAAAGGT GCTTCCCTTC 1320  
 ACAACCACGA CCCTGGACGA CATCCTAAAA TCCTTCTCTG ATGTCAGTGT CATCCGAGTG 1380  
 GCCAGCGGCT ACCTACTGAT GCTTGCTAT GCCTGTTTAA CCATGCTGCG CTGGGACTGC 1440  
 TCCAAGTCCC AGGGTGCCGT GGGGCTGGCT GCGTCCTGT TGGTTGCGCT GTCAGTGGCT 1500  
 GCAGGATTGG GCCTCTGCTC CTTGATTGGC ATTTCTTTA ATGCTGCGAC AACTCAGGTT 1560  
 TTGCCGTTTC TTGCTCTTGG TGTTGGTGTG GATGATGTCT TCCTCCTGGC CCATGCATTC 1620  
 AGTGAAACAG GACAGAATAA GAGGATTCCA TTTGAGGACA GGAATGGGA GTGCCTCAAG 1680

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CGCACCGGAG	CCAGCGTGGC	CCTCACCTCC	ATCAGCAATG	TCACCGCCTT	CTTCATGGCC	1740
GCATTGATCC	CTATCCCTGC	CCTGCGAGCG	TTCTCCCTCC	AGGCTGCTGT	GGTGGTGGTA	1800
TTCAATTTTG	CTATGGTTCT	GCTCATTTTT	CCTGCAATTC	TCAGCATGGA	TTTATACAGA	1860
CGTGAGGACA	GAAGATTGGA	TATTTTCTGC	TGTTTCACAA	GCCCCTGTGT	CAGCAGGGTG	1920
ATTCAAGTTG	AGCCACAGGC	CTACACAGAG	CCTCACAGTA	ACACCCGGTA	CAGCCCCCCA	1980
CCCCCATACA	CCAGCCACAG	CTTCGCCCCAC	GAAACCCATA	TCACTATGCA	GTCCACCGTT	2040
CAGCTCCGCA	CAGAGTATGA	CCCTCACACG	CACGTGTACT	ACACCACCGC	CGAGCCACGC	2100
TCTGAGATCT	CTGTACAGCC	TGTTACCGTC	ACCCAGGACA	ACCTCAGCTG	TCAGAGTCCC	2160
GAGAGCACCA	GCTCTACCAG	GGACCTGCTC	TCCCAGTTCT	CAGACTCCAG	CCTCCACTGC	2220
CTCGAGCCCC	CCTGCACCAA	GTGGACACTC	TCTTCGTTTG	CAGAGAAGCA	CTATGCTCCT	2280
TTCTCCTGA	AACCCAAAGC	CAAGGTTGTG	GTAATCCTTC	TTTTCTGGG	CTTGCTGGGG	2340
GTCAGCCTTT	ATGGGACCAC	CCGAGTGAGA	GACGGGCTGG	ACCTCACGGA	CATTGTTCCC	2400
CGGGAAACCA	GAGAATATGA	CTTCATAGCT	GCCCAGTTCA	AGTACTTCTC	TTTCTACAAC	2460
ATGTATATAG	TCACCCAGAA	AGCAGACTAC	CCGAATATCC	AGCACCTACT	TTACGACCTT	2520
CATAAGAGTT	TCAGCAATGT	GAAGTATGTC	ATGCTGGAGG	AGAACAAGCA	ACTTCCCCAA	2580
ATGTGGCTGC	ACTACTTTAG	AGACTGGCTT	CAAGGACTTC	AGGATGCATT	TGACAGTGAC	2640
TGGGAAACTG	GGAGGATCAT	GCCAAACAAT	TATAAAAATG	GATCAGATGA	CGGGGTCCCTC	2700
GCTTACAAAC	TCCTGGTGCA	GACTGGCAGC	CGAGACAAGC	CCATCGACAT	TAGTCAGTTG	2760
ACTAAACAGC	GTCTGGTAGA	CGCAGATGGC	ATCATTAAATC	CGAGCGCTTT	CTACATCTAC	2820
CTGACCGCTT	GGGTCAGCAA	CGACCCTGTA	GCTTACGCTG	CCTCCCAGGC	CAACATCCGG	2880
CCTCACCGGC	CGGAGTGGGT	CCATGACAAA	GCCGACTACA	TGCCAGAGAC	CAGGCTGAGA	2940
ATCCCAGCAG	CAGAGCCCAT	CGAGTACGCT	CAGTTCCCTT	TCTACCTCAA	CGGCCTACGA	3000
GACACCTCAG	ACTTTGTGGA	AGCCATAGAA	AAAGTGAGAG	TCATCTGTAA	CAACTATACG	3060
AGCCTGGGAC	TGTCCAGCTA	CCCCAATGGC	TACCCCTTCC	TGTTCTGGGA	GCAATACATC	3120
AGCCTGCGCC	ACTGGCTGCT	GCTATCCATC	AGCGTGGTGC	TGGCCTGCAC	GTTTCTAGTG	3180
TGCGCAGTCT	TCCTCCTGAA	CCCCTGGACG	GCCGGGATCA	TTGTCATGGT	CCTGGCTCTG	3240
ATGACCGTTG	AGCTCTTTGG	CATGATGGGC	CTCATTGGGA	TCAAGCTGAG	TGCTGTGCCT	3300
GTGGTCATCC	TGATTGCATC	TGTTGGCATC	GGAGTGGAGT	TCACCGTCCA	CGTGGCTTTG	3360
GCCTTTCTGA	CAGCCATTGG	GGACAAGAAC	CACAGGGCTA	TGCTCGCTCT	GGAACACATG	3420
TTTGCTCCCG	TTCTGGACGG	TGCTGTGTCC	ACTCTGCTGG	GTGTACTGAT	GCTTGCAGGG	3480
TCCGAATTTG	ATTTCAATTGT	CAGATACTTC	TTTGCCGTCC	TGGCCATTCT	CACCGTCTTG	3540
GGGGTTCTCA	ATGGACTGGT	TCTGCTGCCT	GTCCTCTTAT	CCTTCTTTGG	ACCGTGTCTT	3600

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GAGGTGTCTC CAGCCAATGG CCTAAACCGA CTGCCCCACTC CTTGCGCTGA GCCGCCTCCA 3660  
 AGTGTCTGTC GGTTCGCGT GCCTCCTGGT CACACGAACA ATGGGTCTGA TTCCTCCGAC 3720  
 TCGGAGTACA GCTCTCAGAC CACGGTGTCT GGCATCAGTG AGGAGCTCAG GCAATACGAA 3780  
 GCACAGCAGG GTGCCGGAGG CCCTGCCCCAC CAAGTGATTG TGGAAAGCCAC AGAAAACCCCT 3840  
 GTCTTTGCCC GGTCCACTGT GGTCCATCCG GACTCCAGAC ATCAGCCTCC CTTGACCCCT 3900  
 CGGCAACAGC CCCACCTGGA CTCTGGCTCC TTGTCCCCTG GACGGCAAGG CCAGCAGCCT 3960  
 CGAAGGGATC CCCCTAGAGA AGGCTTGCGG CCACCCCCCT ACAGACCGCG CAGAGACGCT 4020  
 TTTGAAATTT CTAAGAAGG GCATTCTGGC CCTAGCAATA GGGACCGCTC AGGGCCCCGT 4080  
 GGGGCCCGTT CTCACAACCC TCGGAACCCA ACGTCCACCG CCATGGGCAG CTCTGTGCCC 4140  
 AGCTACTGCC AGCCCATCAC CACTGTGACG GCTTCTGCTT CGGTGACTGT TGCTGTGCAT 4200  
 CCCCCGCCTG GACCTGGGCG CAACCCCCGA GGGGGGCCCT GTCCAGGCTA TGAGAGCTAC 4260  
 CCTGAGACTG ATCACGGGGT ATTTGAGGAT CCTCATGTGC CTTTTCATGT CAGGTGTGAG 4320  
 AGGAGGGACT CAAAGGTGGA GGTCATAGAG CTACAGGACG TGAATGTGA GGAGAGGCCG 4380  
 TGGGGGAGCA GCTCCAACTG AGGGTAATTA AAATCTGAAG CAAAGAGGCC AAAGATTGGA 4440  
 AAGCCCCGCC CCCACCTCTT TCCAGAACTG CTTGAAGAGA ACTGCTTGGA ATTATGGGAA 4500  
 GGCAGTTCAT TGTTACTGTA ACTGATTGTA TTATTKKGTG AAATATTTCT ATAAATATTT 4560  
 AARAGGTGTA CACATGTAAT ATACATGGAA ATGCTGTACA GTCTATTTCC TGGGGCCTCT 4620  
 CCACTCCTGC CCCAGAGTGG GGAGACCACA GGGGCCCTTT CCCCTGTGTA CATTGGTCTC 4680  
 TGTGCCACAA CCAAGCTTAA CTTAGTTTTA AAAAAAATCT CCCAGCATAT GTCGCTGCTG 4740  
 CTTAAATATT GTATAATTTA CTTGTATAAT TCTATGCAAA TATTGCTTAT GTAATAGGAT 4800  
 TATTTGTAAA GGTTCCTGTT TAAAATATTT TAAATTTGCA TATCACAACC CTGTGGTAGG 4860  
 ATGAATTGTT ACTGTAACT TTTGAACACG CTATGCGTGG TAATTGTTTA ACGAGCAGAC 4920  
 ATGAAGAAAA CAGGTAAATC CCAGTGGCTT CTCTAGGGGT AGTTGTATAT GGTTTCGCATG 4980  
 GGTGGATGTG TGTGTGCATG TGACTTTCCA ATGTACTGTA TTGTGGTTTG TTGTTGTTGT 5040  
 TGCTGTTGTT GTTCATTTTG GTGTTTTTGG TTGCTTTGTA TGATCTTAGC TCTGGCCTAG 5100  
 GTGGGCTGGG AAGGTCCAGG TCTTTTTCTG TCGTGATGCT GGTGGAAAGG TGACCCCAAT 5160  
 CATCTGTCCT ATTCTCTGGG ACTATTC 5187

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1311 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Ala Pro Asp Ser Glu Ala Pro Ser Asn Pro Arg Ile Thr Ala  
1 5 10 15

Ala His Glu Ser Pro Cys Ala Thr Glu Ala Arg His Ser Ala Asp Leu  
20 25 30

Tyr Ile Arg Thr Ser Trp Val Asp Ala Ala Leu Ala Leu Ser Glu Leu  
35 40 45

Glu Lys Gly Asn Ile Glu Gly Gly Arg Thr Ser Leu Trp Ile Arg Ala  
50 55 60

Trp Leu Gln Glu Gln Leu Phe Ile Leu Gly Cys Phe Leu Gln Gly Asp  
65 70 75 80

Ala Gly Lys Val Leu Phe Val Ala Ile Leu Val Leu Ser Thr Phe Cys  
85 90 95

Val Gly Leu Lys Ser Ala Gln Ile His Thr Arg Val Asp Gln Leu Trp  
100 105 110

Val Gln Glu Gly Gly Arg Leu Glu Ala Glu Leu Lys Tyr Thr Ala Gln  
115 120 125

Ala Leu Gly Glu Ala Asp Ser Ser Thr His Gln Leu Val Ile Gln Thr  
130 135 140

Ala Lys Asp Pro Asp Val Ser Leu Leu His Pro Gly Ala Leu Leu Glu  
145 150 155 160

His Leu Lys Val Val His Ala Ala Thr Arg Val Thr Val His Met Tyr  
165 170 175

Asp Ile Glu Trp Arg Leu Lys Asp Leu Cys Tyr Ser Pro Ser Ile Pro  
180 185 190

Asp Phe Glu Gly Tyr His His Ile Glu Ser Ile Ile Asp Asn Val Ile  
195 200 205

Pro Cys Ala Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ser Lys  
210 215 220

Leu Leu Gly Pro Asp Tyr Pro Ile Tyr Val Pro His Leu Lys His Lys  
225 230 235 240

Leu Gln Trp Thr His Leu Asn Pro Leu Glu Val Val Glu Glu Val Lys  
245 250 255

Lys Leu Lys Phe Gln Phe Pro Leu Ser Thr Ile Glu Ala Tyr Met Lys  
260 265 270

Arg Ala Gly Ile Thr Ser Ala Tyr Met Lys Lys Pro Cys Leu Asp Pro  
275 280 285

Thr Asp Pro His Cys Pro Ala Thr Ala Pro Asn Lys Lys Ser Gly His  
290 295 300

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Ile 305	Pro	Asp	Val	Ala 310	Ala	Glu	Leu	Ser	His	Gly 315	Cys	Tyr	Gly	Phe	Ala 320
Ala	Ala	Tyr	Met	His 325	Trp	Pro	Glu	Gln	Leu 330	Ile	Val	Gly	Gly	Ala 335	Thr
Arg	Asn	Ser	Thr 340	Ser	Ala	Leu	Arg	Lys 345	Ala	Arg	Xaa	Leu	Gln 350	Thr	Val
Val	Gln	Leu 355	Met	Gly	Glu	Arg	Glu 360	Met	Tyr	Glu	Tyr	Trp 365	Ala	Asp	His
Tyr	Lys 370	Val	His	Gln	Ile	Gly 375	Trp	Asn	Gln	Glu	Lys 380	Ala	Ala	Ala	Val
Leu 385	Asp	Ala	Trp	Gln	Arg 390	Lys	Phe	Ala	Ala	Glu 395	Val	Arg	Lys	Ile	Thr 400
Thr	Ser	Gly	Ser	Val 405	Ser	Ser	Ala	Tyr	Ser	Phe	Tyr	Pro	Phe	Ser 415	Thr
Ser	Thr	Leu	Asn 420	Asp	Ile	Leu	Gly 425	Lys	Phe	Ser	Glu	Val	Ser 430	Leu	Lys
Asn	Ile	Ile 435	Leu	Gly	Tyr	Met	Phe 440	Met	Leu	Ile	Tyr	Val 445	Ala	Val	Thr
Leu	Ile 450	Gln	Trp	Arg	Asp	Pro 455	Ile	Arg	Ser	Gln	Ala 460	Gly	Val	Gly	Ile
Ala 465	Gly	Val	Leu	Leu	Leu 470	Ser	Ile	Thr	Val	Ala 475	Ala	Gly	Leu	Gly	Phe 480
Cys	Ala	Leu	Leu	Gly 485	Ile	Pro	Phe	Asn	Ala 490	Ser	Ser	Thr	Gln	Ile 495	Val
Pro	Phe	Leu	Ala 500	Leu	Gly	Leu	Gly 505	Val	Gln	Asp	Met	Phe	Leu 510	Leu	Thr
His	Thr	Tyr 515	Val	Glu	Gln	Ala	Gly 520	Asp	Val	Pro	Arg	Glu 525	Glu	Arg	Thr
Gly	Leu 530	Val	Leu	Lys	Lys	Ser 535	Gly	Leu	Ser	Val	Leu 540	Leu	Ala	Ser	Leu
Cys 545	Asn	Val	Met	Ala	Phe 550	Leu	Ala	Ala	Ala	Leu 555	Leu	Pro	Ile	Pro	Ala 560
Phe	Arg	Val	Phe	Cys 565	Leu	Gln	Ala	Ala	Ile 570	Leu	Leu	Leu	Phe	Asn 575	Leu
Gly	Ser	Ile 580	Leu	Leu	Val	Phe	Pro	Ala 585	Met	Ile	Ser	Leu	Asp 590	Leu	Arg
Arg	Arg	Ser 595	Ala	Ala	Arg	Ala	Asp 600	Leu	Leu	Cys	Cys	Leu 605	Met	Pro	Glu
Ser	Pro	Leu	Pro	Lys	Lys	Lys 615	Ile	Pro	Glu	Arg	Ala 620	Lys	Thr	Arg	Lys
Asn 625	Asp	Lys	Thr	His	Arg 630	Ile	Asp	Thr	Thr	Arg 635	Gln	Pro	Leu	Asp	Pro 640

Asp Val Ser Glu Asn Val Thr Lys Thr Cys Cys Leu Ser Val Ser Leu  
 645 650 655  
 Thr Lys Trp Ala Lys Asn Gln Tyr Ala Pro Phe Ile Met Arg Pro Ala  
 660 665 670  
 Val Lys Val Thr Ser Met Leu Ala Leu Ile Ala Val Ile Leu Thr Ser  
 675 680 685  
 Val Trp Gly Ala Thr Lys Val Lys Asp Gly Leu Asp Leu Thr Asp Ile  
 690 695 700  
 Val Pro Glu Asn Thr Asp Glu His Glu Phe Leu Ser Arg Gln Glu Lys  
 705 710 715 720  
 Tyr Phe Gly Phe Tyr Asn Met Tyr Ala Val Thr Gln Gly Asn Phe Glu  
 725 730 735  
 Tyr Pro Thr Asn Gln Lys Leu Leu Tyr Glu Tyr His Asp Gln Phe Val  
 740 745 750  
 Arg Ile Pro Asn Ile Ile Lys Asn Asp Asn Gly Gly Leu Thr Lys Phe  
 755 760 765  
 Trp Leu Ser Leu Phe Arg Asp Trp Leu Leu Asp Leu Gln Val Ala Phe  
 770 775 780  
 Asp Lys Glu Val Ala Ser Gly Cys Ile Thr Gln Glu Tyr Trp Cys Lys  
 785 790 795 800  
 Asn Ala Ser Asp Glu Gly Ile Leu Ala Tyr Lys Leu Met Val Gln Thr  
 805 810 815  
 Gly His Val Asp Asn Pro Ile Asp Lys Ser Leu Ile Thr Ala Gly His  
 820 825 830  
 Arg Leu Val Asp Lys Asp Gly Ile Ile Asn Pro Lys Ala Phe Tyr Asn  
 835 840 845  
 Tyr Leu Ser Ala Trp Ala Thr Asn Asp Ala Leu Ala Tyr Gly Ala Ser  
 850 855 860  
 Gln Gly Asn Leu Lys Pro Gln Pro Gln Arg Trp Ile His Ser Pro Glu  
 865 870 875 880  
 Asp Val His Leu Glu Ile Lys Lys Ser Ser Pro Leu Ile Tyr Thr Gln  
 885 890 895  
 Leu Pro Phe Tyr Leu Ser Gly Leu Ser Asp Thr Xaa Ser Ile Lys Thr  
 900 905 910  
 Leu Ile Arg Ser Val Arg Asp Leu Cys Leu Lys Tyr Glu Ala Lys Gly  
 915 920 925  
 Leu Pro Asn Phe Pro Ser Gly Ile Pro Phe Leu Phe Trp Glu Gln Tyr  
 930 935 940  
 Leu Tyr Leu Arg Thr Ser Leu Leu Leu Ala Leu Ala Cys Ala Leu Ala  
 945 950 955 960  
 Ala Val Phe Ile Ala Val Met Val Leu Leu Leu Asn Ala Trp Ala Ala  
 965 970 975

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Val	Leu	Val	Thr	Leu	Ala	Leu	Ala	Thr	Leu	Val	Leu	Gln	Leu	Gly	
			980					985						990	
Val	Met	Ala	Leu	Leu	Gly	Val	Lys	Leu	Ser	Ala	Met	Pro	Ala	Val	Leu
		995					1000					1005			
Leu	Val	Leu	Ala	Ile	Gly	Arg	Gly	Val	His	Phe	Thr	Val	His	Leu	Cys
		1010				1015					1020				
Leu	Gly	Phe	Val	Thr	Ser	Ile	Gly	Cys	Lys	Arg	Arg	Arg	Ala	Ser	Leu
1025					1030					1035					1040
Ala	Leu	Glu	Ser	Val	Leu	Ala	Pro	Val	Val	His	Gly	Ala	Leu	Ala	Ala
				1045					1050					1055	
Ala	Leu	Ala	Ala	Ser	Met	Leu	Ala	Ala	Ser	Glu	Cys	Gly	Phe	Val	Ala
			1060					1065					1070		
Arg	Leu	Phe	Leu	Arg	Leu	Leu	Leu	Asp	Ile	Val	Phe	Leu	Gly	Leu	Ile
		1075					1080					1085			
Asp	Gly	Leu	Leu	Phe	Phe	Pro	Ile	Val	Leu	Ser	Ile	Leu	Gly	Pro	Ala
	1090					1095					1100				
Ala	Glu	Val	Arg	Pro	Ile	Glu	His	Pro	Glu	Arg	Leu	Ser	Thr	Pro	Ser
1105					1110					1115					1120
Pro	Lys	Cys	Ser	Pro	Ile	His	Pro	Arg	Lys	Ser	Ser	Ser	Ser	Ser	Gly
				1125					1130						1135
Gly	Gly	Asp	Lys	Ser	Ser	Arg	Thr	Ser	Lys	Ser	Ala	Pro	Arg	Pro	Cys
			1140					1145					1150		
Ala	Pro	Ser	Leu	Thr	Thr	Ile	Thr	Glu	Glu	Pro	Ser	Ser	Trp	His	Ser
		1155					1160					1165			
Ser	Ala	His	Ser	Val	Gln	Ser	Ser	Met	Gln	Ser	Ile	Val	Val	Gln	Pro
	1170					1175					1180				
Glu	Val	Val	Val	Glu	Thr	Thr	Thr	Tyr	Asn	Gly	Ser	Asp	Ser	Ala	Ser
1185					1190					1195					1200
Gly	Arg	Ser	Thr	Pro	Thr	Lys	Ser	Ser	His	Gly	Gly	Ala	Ile	Thr	Thr
				1205					1210					1215	
Thr	Lys	Val	Thr	Ala	Thr	Ala	Asn	Ile	Lys	Val	Glu	Val	Val	Thr	Pro
			1220					1225					1230		
Ser	Asp	Arg	Lys	Ser	Arg	Arg	Ser	Tyr	His	Tyr	Tyr	Asp	Arg	Arg	Arg
	1235						1240					1245			
Asp	Arg	Asp	Glu	Asp	Arg	Asp	Arg	Asp	Arg	Glu	Arg	Asp	Arg	Asp	Arg
	1250					1255					1260				
Asp	Arg	Asp	Arg	Asp	Arg	Asp	Arg	Asp	Arg	Asp	Arg	Asp	Arg	Asp	Arg
1265					1270					1275					1280
Glu	Arg	Ser	Arg	Glu	Arg	Asp	Arg	Arg	Asp	Arg	Tyr	Arg	Asp	Glu	Arg
				1285					1290					1295	
Asp	His	Arg	Ala	Ser	Pro	Arg	Glu	Lys	Arg	Gln	Arg	Phe	Trp	Thr	
			1300					1305							

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4434 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAACAAGA GAGCGAGTGA GAGTAGGGAG AGCGTCTGTG TTGTGTGTTG AGTGTCGCCC 60  
 ACGCACACAG GCGCAAAACA GTGCACACAG ACGCCCGCTG GGCAAGAGAG AGTGAGAGAG 120  
 AGAAACAGCG GCGCGCGCTC GCCTAATGAA GTTGTGGGCC TGGCTGGCGT GCCGCATCCA 180  
 CGAGATACAG ATACATCTCT CATGGACCGC GACAGCCTCC CACGCGTTCC GGACACACAC 240  
 GGCGATGTGG TCGATGAGAA ATTATTCTCG GATCTTTACA TACGCACCAG CTGGGTGGAC 300  
 GCGCAAGTGG CGCTCGATCA GATAGATAAG GGCAAAGCGC GTGGCAGCCG CACGGCGATC 360  
 TATCTGCGAT CAGTATTCCA GTCCACCTC GAAACCCTCG GCAGCTCCGT GCAAAAAGCAC 420  
 GCGGGCAAGG TGCTATTCGT GGCTATCCTG GTGCTGAGCA CCTTCTGCGT CGGCCTGAAG 480  
 AGCGCCCAGA TCCACTCCAA GGTGCACCAG CTGTGGATCC AGGAGGGCGG CCGGCTGGAG 540  
 GCGGAACTGG CCTACACACA GAAGACGATC GGCGAGGACG AGTCGGCCAC GCATCAGCTG 600  
 CTCATTGAGA CGACCCACGA CCCGAACGCC TCCGTCCTGC ATCCGCAGGC GCTGCTTGCC 660  
 CACCTGGAGG TCCTGGTCAA GGCCACCGCC GTCAAGGTGC ACCTCTACGA CACCGAATGG 720  
 GGGCTGCGCG ACATGTGCAA CATGCCGAGC ACGCCCTCCT TCGAGGGCAT CTACTACATC 780  
 GAGCAGATCC TGCGCCACCT CATTCCGTGC TCGATCATCA CGCCGCTGGA CTGTTTCTGG 840  
 GAGGGAAGCC AGCTGTTGGG TCCGGAATCA GCGGTCGTTA TACCAGGCCT CAACCAACGA 900  
 CTCCTGTGGA CCACCCTGAA TCCCGCCTCT GTGATGCAGT ATATGAAACA AAAGATGTCC 960  
 GAGGAAAAGA TCAGCTTCGA CTTGAGACC GTGGAGCAGT ACATGAAGCG TCGGGCCATT 1020  
 GGCAGTGGCT ACATGGAGAA GCCCTGCCTG AACCCACTGA ATCCCAATTG CCCGGACACG 1080  
 GCACCGAACA AGAACAGCAC CCAGCCGCCG GATGTGGGAG CCATCCTGTC CGGAGGCTGC 1140  
 TACGGTTATG CCGCGAAGCA CATGCACTGG CCGGAGGAGC TGATTGTGGG CGGACGGAAG 1200  
 AGGAACCGCA GCGGACACTT GAGGAAGGCC CAGGCCCTGC AGTCGGTGGT GCAGCTGATG 1260  
 ACCGAGAAGG AAATGTACGA CCAGTGGCAG GACAACTACA AGGTGCACCA TCTTGATGG 1320  
 ACGCAGGAGA AGGCAGCGGA GGTTTTGAAC GCCTGGCAGC GCAACTTTTC GCGGGAGGTG 1380  
 GAACAGCTGC TACGTAAACA GTCGAGAATT GCCACCAACT ACGATATCTA CGTGTTTCAGC 1440

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TCGGCTGCAC	TGGATGACAT	CCTGGCCAAG	TTCTCCCATC	CCAGCGCCTT	GTCCATTGTC	1500
ATCGGCGTGG	CCGTCACCGT	TTTGTATGCC	TTTTGCACGC	TCCTCCGCTG	GAGGGACCCC	1560
GTCCGTGGCC	AGAGCAGTGT	GGGCGTGGCC	GGAGTTCTGC	TCATGTGCTT	CAGTACCGCC	1620
GCCGGATTGG	GATTGTCAGC	CCTGCTCGGT	ATCGTTTTCA	ATGCGCTGAC	CGCTGCCTAT	1680
GCGGAGAGCA	ATCGGCGGGA	GCAGACCAAG	CTGATTCTCA	AGAACGCCAG	CACCCAGGTG	1740
GTTCCGTTTT	TGGCCCTTGG	TCTGGGCGTC	GATCACATCT	TCATAGTGGG	ACCGAGCATC	1800
CTGTTCAAGT	CCTGCAGCAC	CGCAGGATCC	TTCTTTGCGG	CCGCCTTTAT	TCCGGTGCCG	1860
GCTTTGAAGG	TATTCTGTCT	GCAGGCTGCC	ATCGTAATGT	GCTCCAATTT	GGCAGCGGCT	1920
CTATTGGTTT	TTCCGGCCAT	GATTTCTGTT	GATCTACGGA	GACGTACCGC	CGGCAGGGCG	1980
GACATCTTCT	GCTGCTGTTT	TCCGGTGTGG	AAGGAACAGC	CGAAGGTGGC	ACCTCCGGTG	2040
CTGCCGCTGA	ACAACAACAA	CGGGCGCGGG	GCCCGGCATC	CGAAGAGCTG	CAACAACAAC	2100
AGGGTGCCGC	TGCCCCGCCA	GAATCCTCTG	CTGGAACAGA	GGGCAGACAT	CCCTGGGAGC	2160
AGTCACTCAC	TGGCGTCCTT	CTCCCTGGCA	ACCTTCGCCT	TTCAGCACTA	CACTCCCTTC	2220
CTCATGCGCA	GCTGGGTGAA	GTTCTTGACC	GTTATGGGTT	TCCTGGCGGC	CCTCATATCC	2280
AGCTTGATATG	CCTCCACGCG	CCTTCAGGAT	GGCCTGGACA	TTATTGATCT	GGTGCCCAAG	2340
GACAGCAACG	AGCACAAGTT	CCTGGATGCT	CAAACCTCGC	TCTTTGGCTT	CTACAGCATG	2400
TATGCGGTTA	CCCAGGGCAA	CTTTGAATAT	CCCACCCAGC	AGCAGTTGCT	CAGGGACTAC	2460
CATGATTCCCT	TTGTGCGGGT	GCCACATGTG	ATCAAGAATG	ATAACGGTGG	ACTGCCGGAC	2520
TTCTGGCTGC	TGCTCTTCAG	CGAGTGGCTG	GGTAATCTGC	AAAAGATATT	CGACGAGGAA	2580
TACCGCGACG	GACGGCTGAC	CAAGGAGTGC	TGGTTCCCAA	ACGCCAGCAG	CGATGCCATC	2640
CTGGCCTACA	AGCTAATCGT	GCAAACCGGC	CATGTGGACA	ACCCCGTGGA	CAAGGAACTG	2700
GTGCTCACCA	ATCGCCTGGT	CAACAGCGAT	GGCATCATCA	ACCAACGCGC	CTTCTACAAC	2760
TATCTGTCGG	CATGGGCCAC	CAACGACGTC	TTCGCCTACG	GAGCTTCTCA	GGGCAAATTG	2820
TATCCGGAAC	CGCGCCAGTA	TTTTACCAA	CCCAACGAGT	ACGATCTTAA	GATACCCAAG	2880
AGTCTGCCAT	TGGTCTACGC	TCAGATGCCC	TTTTACCTCC	ACGGAATAAC	AGATACCTCG	2940
CAGATCAAGA	CCCTGATAGG	TCATATTCGC	GACCTGAGCG	TCAAGTACGA	GGGCTTCGGC	3000
CTGCCCAACT	ATCCATCGGG	CATTCCCTTC	ATCTTCTGGG	AGCAGTACAT	GACCCTGCGC	3060
TCCTCACTGG	CCATGATCCT	GGCCTGCGTG	CTACTCGCCG	CCCTGGTGCT	GGTCTCCCTG	3120
CTCCTGCTCT	CCGTTTGGGC	CGCCGTTCTC	GTGATCCTCA	GCGTTCTGGC	CTCGCTGGCC	3180
CAGATCTTTG	GGGCCATGAC	TCTGCTGGGC	ATCAAACCTCT	CGGCCATTCC	GGCAGTCATA	3240
CTCATCCTCA	GCGTGGGCAT	GATGCTGTGC	TTCAATGTGC	TGATATCACT	GGGCTTCATG	3300
ACATCCGTTG	GCAACCGACA	GCGCCGCGTC	CAGCTGAGCA	TGCAGATGTC	CCTGGGACCA	3360

CTTGTCCACG GCATGCTGAC CTCCGGAGTG GCCGTGTTCA TGCTCTCCAC GTCGCCCTTT 3420  
 GAGTTTGTGA TCCGGCACTT CTGCTGGCTT CTGCTGGTGG TCTTATGCGT TGGCGCCTGC 3480  
 AACAGCCTTT TGGTGTTCCT CATCCTACTG AGCATGGTGG GACCGGAGGC GGAGCTGGTG 3540  
 CCGCTGGAGC ATCCAGACCG CATATCCACG CCCTCTCCGC TGCCCGTGCG CAGCAGCAAG 3600  
 AGATCGGGCA AATCCTATGT GGTGCAGGGA TCGCGATCCT CGCGAGGCAG CTGCCAGAAG 3660  
 TCGCATCACC ACCACCACAA AGACCTTAAT GATCCATCGC TGACGACGAT CACCGAGGAG 3720  
 CCGCAGTCGT GGAAGTCCAG CAACTCGTCC ATCCAGATGC CCAATGATTG GACCTACCAG 3780  
 CCGCGGGGAA AGCGACCCGC CTCCTACGCG GCGCCGCCCC CCGCCTATCA CAAGGCCGCC 3840  
 GCCCAGCAGC ACCACCAGCA TCAGGGCCCG CCCACAACGC CCGCGCCTCC CTTCCCGACG 3900  
 GCCTATCCGC CGGAGCTGCA GAGCATCGTG GTGCAGCCGG AGGTGACGGT GGAGACGACG 3960  
 CACTCGGACA GCAACACCAC CAAGGTGACG GCCACGGCCA ACATCAAGGT GGAGCTGGCC 4020  
 ATGCCCCGCA GGGCGGTGCG CAGCTATAAC TTTACGAGTT AGCACTAGCA CTAGTTCCTG 4080  
 TAGCTATTAG GACGTATCTT TAGACTCTAG CCTAAGCCGT AACCCTATTT GTATCTGTAA 4140  
 AATCGATTTG TCCAGCGGGT CTGCTGAGGA TTTCGTTCTC ATGGATTCTC ATGGATTCTC 4200  
 ATGGATGCTT AAATGGCATG GTAATTGGCA AAATATCAAT TTTTGTGTCT CAAAAAGATG 4260  
 CATTAGCTTA TGGTTTCAAG ATACATTTTT AAAGAGTCCG CCAGATATTT ATATAAAAAA 4320  
 AATCCAAAAT CGACGTATCC ATGAAAATTG AAAAGCTAAG CAGACCCGTA TGTATGTATA 4380  
 TGTGTATGCA TGTTAGTTAA TTTCCCGAAG TCCGGTATTT ATAGCAGCTG CCTT 4434

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1285 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Arg	Asp	Ser	Leu	Pro	Arg	Val	Pro	Asp	Thr	His	Gly	Asp	Val
1				5					10					15	
Val	Asp	Glu	Lys	Leu	Phe	Ser	Asp	Leu	Tyr	Ile	Arg	Thr	Ser	Trp	Val
		20						25					30		
Asp	Ala	Gln	Val	Ala	Leu	Asp	Gln	Ile	Asp	Lys	Gly	Lys	Ala	Arg	Gly
		35					40					45			
Ser	Arg	Thr	Ala	Ile	Tyr	Leu	Arg	Ser	Val	Phe	Gln	Ser	His	Leu	Glu
		50					55				60				

09916140-082197

Thr Leu Gly Ser Ser Val Gln Lys His Ala Gly Lys Val Leu Phe Val  
 65 70 75 80  
 Ala Ile Leu Val Leu Ser Thr Phe Cys Val Gly Leu Lys Ser Ala Gln  
 85 90 95  
 Ile His Ser Lys Val His Gln Leu Trp Ile Gln Glu Gly Gly Arg Leu  
 100 105 110  
 Glu Ala Glu Leu Ala Tyr Thr Gln Lys Thr Ile Gly Glu Asp Glu Ser  
 115 120 125  
 Ala Thr His Gln Leu Leu Ile Gln Thr Thr His Asp Pro Asn Ala Ser  
 130 135 140  
 Val Leu His Pro Gln Ala Leu Leu Ala His Leu Glu Val Leu Val Lys  
 145 150 155 160  
 Ala Thr Ala Val Lys Val His Leu Tyr Asp Thr Glu Trp Gly Leu Arg  
 165 170 175  
 Asp Met Cys Asn Met Pro Ser Thr Pro Ser Phe Glu Gly Ile Tyr Tyr  
 180 185 190  
 Ile Glu Gln Ile Leu Arg His Leu Ile Pro Cys Ser Ile Ile Thr Pro  
 195 200 205  
 Leu Asp Cys Phe Trp Glu Gly Ser Gln Leu Leu Gly Pro Glu Ser Ala  
 210 215 220  
 Val Val Ile Pro Gly Leu Asn Gln Arg Leu Leu Trp Thr Thr Leu Asn  
 225 230 235 240  
 Pro Ala Ser Val Met Gln Tyr Met Lys Gln Lys Met Ser Glu Glu Lys  
 245 250 255  
 Ile Ser Phe Asp Phe Glu Thr Val Glu Gln Tyr Met Lys Arg Ala Ala  
 260 265 270  
 Ile Gly Ser Gly Tyr Met Glu Lys Pro Cys Leu Asn Pro Leu Asn Pro  
 275 280 285  
 Asn Cys Pro Asp Thr Ala Pro Asn Lys Asn Ser Thr Gln Pro Pro Asp  
 290 295 300  
 Val Gly Ala Ile Leu Ser Gly Gly Cys Tyr Gly Tyr Ala Ala Lys His  
 305 310 315 320  
 Met His Trp Pro Glu Glu Leu Ile Val Gly Gly Arg Lys Arg Asn Arg  
 325 330 335  
 Ser Gly His Leu Arg Lys Ala Gln Ala Leu Gln Ser Val Val Gln Leu  
 340 345 350  
 Met Thr Glu Lys Glu Met Tyr Asp Gln Trp Gln Asp Asn Tyr Lys Val  
 355 360 365  
 His His Leu Gly Trp Thr Gln Glu Lys Ala Ala Glu Val Leu Asn Ala  
 370 375 380  
 Trp Gln Arg Asn Phe Ser Arg Glu Val Glu Gln Leu Leu Arg Lys Gln  
 385 390 395 400

03916140-032197

Ser Arg Ile Ala Thr Asn Tyr Asp Ile Tyr Val Phe Ser Ser Ala Ala  
 405 410 415  
 Leu Asp Asp Ile Leu Ala Lys Phe Ser His Pro Ser Ala Leu Ser Ile  
 420 425 430  
 Val Ile Gly Val Ala Val Thr Val Leu Tyr Ala Phe Cys Thr Leu Leu  
 435 440 445  
 Arg Trp Arg Asp Pro Val Arg Gly Gln Ser Ser Val Gly Val Ala Gly  
 450 455 460  
 Val Leu Leu Met Cys Phe Ser Thr Ala Ala Gly Leu Gly Leu Ser Ala  
 465 470 475 480  
 Leu Leu Gly Ile Val Phe Asn Ala Leu Thr Ala Ala Tyr Ala Glu Ser  
 485 490 495  
 Asn Arg Arg Glu Gln Thr Lys Leu Ile Leu Lys Asn Ala Ser Thr Gln  
 500 505 510  
 Val Val Pro Phe Leu Ala Leu Gly Leu Gly Val Asp His Ile Phe Ile  
 515 520 525  
 Val Gly Pro Ser Ile Leu Phe Ser Ala Cys Ser Thr Ala Gly Ser Phe  
 530 535 540  
 Phe Ala Ala Ala Phe Ile Pro Val Pro Ala Leu Lys Val Phe Cys Leu  
 545 550 555 560  
 Gln Ala Ala Ile Val Met Cys Ser Asn Leu Ala Ala Ala Leu Leu Val  
 565 570 575  
 Phe Pro Ala Met Ile Ser Leu Asp Leu Arg Arg Arg Thr Ala Gly Arg  
 580 585 590  
 Ala Asp Ile Phe Cys Cys Cys Phe Pro Val Trp Lys Glu Gln Pro Lys  
 595 600 605  
 Val Ala Pro Pro Val Leu Pro Leu Asn Asn Asn Asn Gly Arg Gly Ala  
 610 615 620  
 Arg His Pro Lys Ser Cys Asn Asn Asn Arg Val Pro Leu Pro Ala Gln  
 625 630 635 640  
 Asn Pro Leu Leu Glu Gln Arg Ala Asp Ile Pro Gly Ser Ser His Ser  
 645 650 655  
 Leu Ala Ser Phe Ser Leu Ala Thr Phe Ala Phe Gln His Tyr Thr Pro  
 660 665 670  
 Phe Leu Met Arg Ser Trp Val Lys Phe Leu Thr Val Met Gly Phe Leu  
 675 680 685  
 Ala Ala Leu Ile Ser Ser Leu Tyr Ala Ser Thr Arg Leu Gln Asp Gly  
 690 695 700  
 Leu Asp Ile Ile Asp Leu Val Pro Lys Asp Ser Asn Glu His Lys Phe  
 705 710 715 720  
 Leu Asp Ala Gln Thr Arg Leu Phe Gly Phe Tyr Ser Met Tyr Ala Val  
 725 730 735  
 Thr Gln Gly Asn Phe Glu Tyr Pro Thr Gln Gln Gln Leu Leu Arg Asp

08916140-082197

740										745										750										
Tyr	His	Asp	Ser	Phe	Arg	Val	Pro	His	Val	Ile	Lys	Asn	Asp	Asn	Gly															
		755					760					765																		
Gly	Leu	Pro	Asp	Phe	Trp	Leu	Leu	Leu	Phe	Ser	Glu	Trp	Leu	Gly	Asn															
	770					775					780																			
Leu	Gln	Lys	Ile	Phe	Asp	Glu	Glu	Tyr	Arg	Asp	Gly	Arg	Leu	Thr	Lys															
785					790					795					800															
Glu	Cys	Trp	Phe	Pro	Asn	Ala	Ser	Ser	Asp	Ala	Ile	Leu	Ala	Tyr	Lys															
				805					810					815																
Leu	Ile	Val	Gln	Thr	Gly	His	Val	Asp	Asn	Pro	Val	Asp	Lys	Glu	Leu															
			820					825					830																	
Val	Leu	Thr	Asn	Arg	Leu	Val	Asn	Ser	Asp	Gly	Ile	Ile	Asn	Gln	Arg															
		835					840						845																	
Ala	Phe	Tyr	Asn	Tyr	Leu	Ser	Ala	Trp	Ala	Thr	Asn	Asp	Val	Phe	Ala															
		850				855					860																			
Tyr	Gly	Ala	Ser	Gln	Gly	Lys	Leu	Tyr	Pro	Glu	Pro	Arg	Gln	Tyr	Phe															
865					870					875					880															
His	Gln	Pro	Asn	Glu	Tyr	Asp	Leu	Lys	Ile	Pro	Lys	Ser	Leu	Pro	Leu															
				885					890					895																
Val	Tyr	Ala	Gln	Met	Pro	Phe	Tyr	Leu	His	Gly	Leu	Thr	Asp	Thr	Ser															
			900					905					910																	
Gln	Ile	Lys	Thr	Leu	Ile	Gly	His	Ile	Arg	Asp	Leu	Ser	Val	Lys	Tyr															
		915					920					925																		
Glu	Gly	Phe	Gly	Leu	Pro	Asn	Tyr	Pro	Ser	Gly	Ile	Pro	Phe	Ile	Phe															
	930					935					940																			
Trp	Glu	Gln	Tyr	Met	Thr	Leu	Arg	Ser	Ser	Leu	Ala	Met	Ile	Leu	Ala															
945					950					955					960															
Cys	Val	Leu	Leu	Ala	Ala	Leu	Val	Leu	Val	Ser	Leu	Leu	Leu	Leu	Ser															
				965					970					975																
Val	Trp	Ala	Ala	Val	Leu	Val	Ile	Leu	Ser	Val	Leu	Ala	Ser	Leu	Ala															
			980					985					990																	
Gln	Ile	Phe	Gly	Ala	Met	Thr	Leu	Leu	Gly	Ile	Lys	Leu	Ser	Ala	Ile															
		995					1000					1005																		
Pro	Ala	Val	Ile	Leu	Ile	Leu	Ser	Val	Gly	Met	Met	Leu	Cys	Phe	Asn															
		1010				1015					1020																			
Val	Leu	Ile	Ser	Leu	Gly	Phe	Met	Thr	Ser	Val	Gly	Asn	Arg	Gln	Arg															
1025					1030					1035					1040															
Arg	Val	Gln	Leu	Ser	Met	Gln	Met	Ser	Leu	Gly	Pro	Leu	Val	His	Gly															
				1045					1050					1055																
Met	Leu	Thr	Ser	Gly	Val	Ala	Val	Phe	Met	Leu	Ser	Thr	Ser	Pro	Phe															
			1060					1065					1070																	
Glu	Phe	Val	Ile	Arg	His	Phe	Cys	Trp	Leu	Leu	Leu	Val	Val	Leu	Cys															

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1075                      1080                      1085

Val Gly Ala Cys Asn Ser Leu Leu Val Phe Pro Ile Leu Leu Ser Met  
1090                      1095                      1100

Val Gly Pro Glu Ala Glu Leu Val Pro Leu Glu His Pro Asp Arg Ile  
1105                      1110                      1115                      1120

Ser Thr Pro Ser Pro Leu Pro Val Arg Ser Ser Lys Arg Ser Gly Lys  
1125                      1130                      1135

Ser Tyr Val Val Gln Gly Ser Arg Ser Ser Arg Gly Ser Cys Gln Lys  
1140                      1145                      1150

Ser His His His His His Lys Asp Leu Asn Asp Pro Ser Leu Thr Thr  
1155                      1160                      1165

Ile Thr Glu Glu Pro Gln Ser Trp Lys Ser Ser Asn Ser Ser Ile Gln  
1170                      1175                      1180

Met Pro Asn Asp Trp Thr Tyr Gln Pro Arg Glu Gln Arg Pro Ala Ser  
1185                      1190                      1195                      1200

Tyr Ala Ala Pro Pro Pro Ala Tyr His Lys Ala Ala Ala Gln Gln His  
1205                      1210                      1215

His Gln His Gln Gly Pro Pro Thr Thr Pro Pro Pro Pro Phe Pro Thr  
1220                      1225                      1230

Ala Tyr Pro Pro Glu Leu Gln Ser Ile Val Val Gln Pro Glu Val Thr  
1235                      1240                      1245

Val Glu Thr Thr His Ser Asp Ser Asn Thr Thr Lys Val Thr Ala Thr  
1250                      1255                      1260

Ala Asn Ile Lys Val Glu Leu Ala Met Pro Gly Arg Ala Val Arg Ser  
1265                      1270                      1275                      1280

Tyr Asn Phe Thr Ser  
1285

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGGTCCATC AGCTTTGGAT ACAGGAAGGT GGTTCGCTCG AGCATGAGCT AGCCTACACG	60
CAGAAATCGC TCGGCGAGAT GGACTCCTCC ACGCACCAGC TGCTAATCCA AACNCCCCAA	120
GATATGGACG CCTCGATACT GCACCCGAAC GCGCTACTGA CGCACCTGGA CGTGGTGAAG	180
AAAGCGATCT CGGTGACGGT GCACATGTAC GACATCACGT GGAGNCTCAA GGACATGTGC	240

08915140-082197



TACTCGCCCA GCATACCGAG NTTCGATACG CACTTTATCG AGCAGATCTT CGAGAACATC 300  
 ATACCGTGCG CGATCATCAC GCCGCTGGAT TGCTTTTGGG AGGGA 345

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Val His Gln Leu Trp Ile Gln Glu Gly Gly Ser Leu Glu His Glu  
 1 5 10 15  
 Leu Ala Tyr Thr Gln Lys Ser Leu Gly Glu Met Asp Ser Ser Thr His  
 20 25 30  
 Gln Leu Leu Ile Gln Thr Pro Lys Asp Met Asp Ala Ser Ile Leu His  
 35 40 45  
 Pro Asn Ala Leu Leu Thr His Leu Asp Val Val Lys Lys Ala Ile Ser  
 50 55 60  
 Val Thr Val His Met Tyr Asp Ile Thr Trp Xaa Leu Lys Asp Met Cys  
 65 70 75 80  
 Tyr Ser Pro Ser Ile Pro Xaa Phe Asp Thr His Phe Ile Glu Gln Ile  
 85 90 95  
 Phe Glu Asn Ile Ile Pro Cys Ala Ile Ile Thr Pro Leu Asp Cys Phe  
 100 105 110  
 Trp Glu Gly  
 115

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5187 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTCTGTCA CCCGAGCCG GAGTCCCCGG CGGCCAGCAG CGTCCTCGCG AGCCGAGCGC 60  
 CCAGGCGCGC CCGGAGCCG CGGCGGCGGC GGCAACATGG CCTCGGCTGG TAACGCCGCC 120

2675140-02249

GGGGCCCTGG GCAGGCAGGC CGGCGGCGGG AGGCGCAGAC GGACCGGGGG ACCGCACCGC 180  
GCCGCGCCGG ACCGGGACTA TCTGCACCGG CCCAGCTACT GCGACGCCGC CTTCGCTCTG 240  
GAGCAGATTT CCAAGGGGAA GGCTACTGGC CGGAAAGCGC CGCTGTGGCT GAGAGCGAAG 300  
TTTCAGAGAC TCTTATTTAA ACTGGGTTGT TACATTCAA AGAACTGCGG CAAGTTTTTG 360  
GTTGTGGGTC TCCTCATATT TGGGGCCTTC GCTGTGGGAT TAAAGGCAGC TAATCTCGAG 420  
ACCAACGTGG AGGAGCTGTG GGTGGAAGTT GGTGGACGAG TGAGTCGAGA ATTAAATTAT 480  
ACCCGTCAGA AGATAGGAGA AGAGGCTATG TTTAATCCTC AACTCATGAT ACAGACTCCA 540  
AAAGAAGAAG GCGCTAATGT TCTGACCACA GAGGCTCTCC TGCAACACCT GGAATCAGCA 600  
CTCCAGGCCA GTCGTGTGCA CGTCTACATG TATAACAGGC AATGGAAGTT GGAACATTTG 660  
TGCTACAAAT CAGGGGAACT TATCACGGAG ACAGGTTACA TGGATCAGAT AATAGAATAC 720  
CTTTACCCTT GCTTAATCAT TACACCTTTG GACTGCTTCT GGAAGGGGC AAAGCTACAG 780  
TCGGGGACAG CATACTCCT AGGTAAGCCT CCTTTACGGT GGACAACTT TGACCCCTTG 840  
GAATTCCTAG AAGAGTTAAA GAAAATAAAC TACCAAGTGG ACAGCTGGGA GGAAATGCTG 900  
AATAAAGCCG AAGTTGGCCA TGGGTACATG GACCGGCCTT GCCTCAACCC AGCCGACCCA 960  
GATTGCCCTG CCACAGCCCC TAACAAAAAT TCAACCAAAC CTCTTGATGT GGCCCTTGTT 1020  
TTGAATGGTG GATGTCAAGG TTTATCCAGG AAGTATATGC ATTGGCAGGA GGAGTTGATT 1080  
GTGGGTGGTA CCGTCAAGAA TGCCACTGGA AAAGTTGTCA GCGCTCACGC CCTGCAAACC 1140  
ATGTTCCAGT TAATGACTCC CAAGCAAATG TATGAACACT TCAGGGGCTA CGACTATGTC 1200  
TCTCACATCA ACTGGAATGA AGACAGGGCA GCCGCCATCC TGGAGGCCTG GCAGAGGACT 1260  
TACGTGGAGG TGGTTCATCA AAGTGTCGCC CCAAACCTCA CTCAAAGGT GCTTCCCTTC 1320  
ACAACCACGA CCCTGGACGA CATCCTAAAA TCCTTCTCTG ATGTCAGTGT CATCCGAGTG 1380  
GCCAGCGGCT ACCTACTGAT GCTTGCCTAT GCCTGTTTAA CCATGCTGCG CTGGGACTGC 1440  
TCCAAGTCCC AGGGTGCCGT GGGGCTGGCT GGCCTCCTGT TGGTTGCGCT GTCAGTGGCT 1500  
GCAGGATTGG GCCTCTGCTC CTGATTGGC ATTTCTTTTA ATGCTGCGAC AACTCAGGTT 1560  
TTGCCGTTTC TTGCTCTTGG TGTGTTGTG GATGATGTCT TCCTCCTGGC CCATGCATTC 1620  
AGTGAAACAG GACAGAATAA GAGGATTCCA TTTGAGGACA GGACTGGGGA GTGCCTCAAG 1680  
CGCACCGGAG CCAGCGTGGC CCTCACCTCC ATCAGCAATG TCACCGCCTT CTTTATGGCC 1740  
GCATTGATCC CTATCCCTGC CCTGCGAGCG TTCTCCCTCC AGGCTGCTGT GGTGGTGGTA 1800  
TTCAATTTTG CTATGGTTCT GCTCATTTTT CCTGCAATTC TCAGCATGGA TTTATACAGA 1860  
CGTGAGGACA GAAGATTGGA TATTTTCTGC TGTTTCACAA GCCCCTGTGT CAGCAGGGTG 1920  
ATTCAAGTTG AGCCACAGGC CTACACAGAG CCTCACAGTA ACACCCGGTA CAGCCCCCA 1980  
CCCCATACA CCAGCCACAG CTTCGCCAC GAAACCCATA TCACTATGCA GTCCACCGTT 2040

08915140-082197

CAGCTCCGCA CAGAGTATGA CCCTCACACG CACGTGTACT ACACCACCGC CGAGCCACGC	2100
TCTGAGATCT CTGTACAGCC TGTTACCGTC ACCCAGGACA ACCTCAGCTG TCAGAGTCCC	2160
GAGAGCACCA GCTCTACCAG GGACCTGCTC TCCCAGTTCT CAGACTCCAG CCTCCACTGC	2220
CTCGAGCCCC CCTGCACCAA GTGGACACTC TCTTCGTTTG CAGAGAAGCA CTATGCTCCT	2280
TTCCTCCTGA AACCCAAAGC CAAGGTTGTG GTAATCCTTC TTTTCCTGGG CTTGCTGGGG	2340
GTCAGCCTTT ATGGGACCAC CCGAGTGAGA GACGGGCTGG ACCTCACGGA CATTGTTCCC	2400
CGGGAAACCA GAGAATATGA CTTCATAGCT GCCCAGTTCA AGTACTTCTC TTTCTACAAC	2460
ATGTATATAG TCACCCAGAA AGCAGACTAC CCGAATATCC AGCACCTACT TTACGACCTT	2520
CATAAGAGTT TCAGCAATGT GAAGTATGTC ATGCTGGAGG AGAACAAGCA ACTTCCCCAA	2580
ATGTGGCTGC ACTACTTTAG AGACTGGCTT CAAGGACTTC AGGATGCATT TGACAGTGAC	2640
TGGGAAACTG GGAGGATCAT GCCAAACAAT TATAAAAATG GATCAGATGA CGGGGTCTC	2700
GCTTACAAAC TCCTGGTGCA GACTGGCAGC CGAGACAAGC CCATCGACAT TAGTCAGTTG	2760
ACTAAACAGC GTCTGGTAGA CGCAGATGGC ATCATTAAATC CGAGCGCTTT CTACATCTAC	2820
CTGACCGCTT GGGTCAGCAA CGACCCTGTA GCTTACGCTG CCTCCCAGGC CAACATCCGG	2880
CCTCACCGGC CGGAGTGGGT CCATGACAAA GCCGACTACA TGCCAGAGAC CAGGCTGAGA	2940
ATCCCAGCAG CAGAGCCCAT CGAGTACGCT CAGTTCCCTT TCTACCTCAA CGGCCTACGA	3000
GACACCTCAG ACTTTGTGGA AGCCATAGAA AAAGTGAGAG TCATCTGTAA CAACTATACG	3060
AGCCTGGGAC TGTCCAGCTA CCCCAATGGC TACCCCTTCC TGTTCTGGGA GCAATACATC	3120
AGCCTGCGCC ACTGGCTGCT GCTATCCATC AGCGTGGTGC TGGCCTGCAC GTTTCTAGTG	3180
TGCGCAGTCT TCCTCCTGAA CCCCTGGACG GCCGGGATCA TTGTCATGGT CCTGGCTCTG	3240
ATGACCGTTG AGCTCTTTGG CATGATGGGC CTCATTGGGA TCAAGCTGAG TGCTGTGCCT	3300
GTGGTCATCC TGATTGCATC TGTTGGCATC GGAGTGGAGT TCACCGTCCA CGTGGCTTTG	3360
GCCTTTCTGA CAGCCATTGG GGACAAGAAC CACAGGGCTA TGCTCGCTCT GGAACACATG	3420
TTTGCTCCCG TTCTGGACGG TGCTGTGTCC ACTCTGCTGG GTGTACTGAT GCTTGCAGGG	3480
TCCGAATTTG ATTTTCATTGT CAGATACTTC TTTGCCGTCC TGGCCATTCT CACCGTCTTG	3540
GGGGTTCTCA ATGGACTGGT TCTGCTGCCT GTCCTCTTAT CCTTCTTTGG ACCGTGTCCT	3600
GAGGTGTCTC CAGCCAATGG CCTAAACCGA CTGCCCACTC CTTGCGCTGA GCCGCCTCCA	3660
AGTGTCGTCC GGTTCGCCGT GCCTCCTGGT CACACGAACA ATGGGTCTGA TTCCTCCGAC	3720
TCGGAGTACA GCTCTCAGAC CACGGTGTCT GGCATCAGTG AGGAGCTCAG GCAATACGAA	3780
GCACAGCAGG GTGCCGGAGG CCCTGCCCCAC CAAGTGATTG TGGAAGCCAC AGAAAACCCT	3840
GTCTTTGCCC GGTCCACTGT GGTCCATCCG GACTCCAGAC ATCAGCCTCC CTTGACCCCT	3900

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CGGCAACAGC CCCACCTGGA CTCTGGCTCC TTGTCCCCTG GACGGCAAGG CCAGCAGCCT 3960  
 CGAAGGGATC CCCCTAGAGA AGGCTTGCGG CCACCCCCCT ACAGACCGCG CAGAGACGCT 4020  
 TTTGAAATTT CTA CTGAAGG GCATTCTGGC CCTAGCAATA GGGACCGCTC AGGGCCCCGT 4080  
 GGGGGCCGTT CTCACAACCC TCGGAACCCA ACGTCCACCG CCATGGGCAG CTCTGTGCCC 4140  
 AGCTACTGCC AGCCCATCAC CACTGTGACG GCTTCTGCTT CGGTGACTGT TGCTGTGCAT 4200  
 CCCCCGCTG GACCTGGGCG CAACCCCCGA GGGGGGCCCT GTCCAGGCTA TGAGAGCTAC 4260  
 CCTGAGACTG ATCACGGGT ATTTGAGGAT CCTCATGTGC CTTTTCATGT CAGGTGTGAG 4320  
 AGGAGGGACT CAAAGGTGGA GGTCATAGAG CTACAGGACG TGAATGTGA GGAGAGGCCG 4380  
 TGGGGGAGCA GCTCCTACTG AGGGTAATTA AAATCTGAAG CAAAGAGGCC AAAGATTGGA 4440  
 AAGCCCCGCC CCCACCTCTT TCCAGAAGT CTTGAAGAGA ACTGCTTGGA ATTATGGGAA 4500  
 GGCAGTTCAT TGTTACTGTA ACTGATTGTA TTATTKKGTG AAATATTTCT ATAAATATTT 4560  
 AARAGGTGTA CACATGTAAT ATACATGGAA ATGCTGTACA GTCTATTTCC TGGGGCCTCT 4620  
 CCACTCCTGC CCCAGAGTGG GGAGACCACA GGGGCCCTTT CCCCTGTGTA CATTGGTCTC 4680  
 TGTGCCACAA CCAAGCTTAA CTTAGTTTTA AAAAAAATCT CCCAGCATAT GTCGCTGCTG 4740  
 CTTAAATATT GTATAATTTA CTTGTATAAT TCTATGCAAA TATTGCTTAT GTAATAGGAT 4800  
 TATTTGTAAA GGTTCCTGTT TAAATATTT TAAATTTGCA TATCACAACC CTGTGGTAGG 4860  
 ATGAATTGTT ACTGTAACT TTTGAACACG CTATGCGTGG TAATTGTTTA ACGAGCAGAC 4920  
 ATGAAGAAAA CAGGTTAATC CCAGTGGCTT CTCTAGGGGT AGTTGTATAT GGTTCGCATG 4980  
 GGTGGATGTG TGTGTGCATG TGACTTTCCA ATGTACTGTA TTGTGGTTTG TTGTTGTTGT 5040  
 TGCTGTTGTT GTTCATTTTG GTGTTTTTGG TTGCTTTGTA TGATCTTAGC TCTGGCCTAG 5100  
 GTGGGCTGGG AAGGTCCAGG TCTTTTCTG TCGTGATGCT GGTGGAAAGG TGACCCCAAT 5160  
 CATCTGTCCT ATTCTCTGGG ACTATTC 5187

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1434 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Ser Ala Gly Asn Ala Ala Gly Ala Leu Gly Arg Gln Ala Gly  
 1 5 10 15  
 Gly Gly Arg Arg Arg Arg Thr Gly Gly Pro His Arg Ala Ala Pro Asp

20 25 30  
 Arg Asp Tyr Leu His Arg Pro Ser Tyr Cys Asp Ala Ala Phe Ala Leu  
 35 40 45  
 Glu Gln Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp  
 50 55 60  
 Leu Arg Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile  
 65 70 75 80  
 Gln Lys Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly  
 85 90 95  
 Ala Phe Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu  
 100 105 110  
 Glu Leu Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr  
 115 120 125  
 Thr Arg Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met  
 130 135 140  
 Ile Gln Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala  
 145 150 155 160  
 Leu Leu Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val  
 165 170 175  
 Tyr Met Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser  
 180 185 190  
 Gly Glu Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr  
 195 200 205  
 Leu Tyr Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly  
 210 215 220  
 Ala Lys Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu  
 225 230 235 240  
 Arg Trp Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys  
 245 250 255  
 Ile Asn Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu  
 260 265 270  
 Val Gly His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro  
 275 280 285  
 Asp Cys Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp  
 290 295 300  
 Val Ala Leu Val Leu Asn Gly Gly Cys Gln Gly Leu Ser Arg Lys Tyr  
 305 310 315 320  
 Met His Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ala  
 325 330 335  
 Thr Gly Lys Leu Val Ser Ala His Ala Leu Gln Thr Met Phe Gln Leu  
 340 345 350  
 Met Thr Pro Lys Gln Met Tyr Glu His Phe Arg Gly Tyr Asp Tyr Val  
 355 360 365

00915440-002197

Ser His Ile Asn Trp Asn Glu Asp Arg Ala Ala Ala Ile Leu Glu Ala  
 370 375 380  
 Trp Gln Arg Thr Tyr Val Glu Val Val His Gln Ser Val Ala Pro Asn  
 385 390 395 400  
 Ser Thr Gln Lys Val Leu Pro Phe Thr Thr Thr Thr Leu Asp Asp Ile  
 405 410 415  
 Leu Lys Ser Phe Ser Asp Val Ser Val Ile Arg Val Ala Ser Gly Tyr  
 420 425 430  
 Leu Leu Met Leu Ala Tyr Ala Cys Leu Thr Met Leu Arg Trp Asp Cys  
 435 440 445  
 Ser Lys Ser Gln Gly Ala Val Gly Leu Ala Gly Val Leu Leu Val Ala  
 450 455 460  
 Leu Ser Val Ala Ala Gly Leu Gly Leu Cys Ser Leu Ile Gly Ile Ser  
 465 470 475 480  
 Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly Val  
 485 490 495  
 Gly Val Asp Asp Val Phe Leu Leu Ala His Ala Phe Ser Glu Thr Gly  
 500 505 510  
 Gln Asn Lys Arg Ile Pro Phe Glu Asp Arg Thr Gly Glu Cys Leu Lys  
 515 520 525  
 Arg Thr Gly Ala Ser Val Ala Leu Thr Ser Ile Ser Asn Val Thr Ala  
 530 535 540  
 Phe Phe Met Ala Ala Leu Ile Pro Ile Pro Ala Leu Arg Ala Phe Ser  
 545 550 555 560  
 Leu Gln Ala Ala Val Val Val Val Phe Asn Phe Ala Met Val Leu Leu  
 565 570 575  
 Ile Phe Pro Ala Ile Leu Ser Met Asp Leu Tyr Arg Arg Glu Asp Arg  
 580 585 590  
 Arg Leu Asp Ile Phe Cys Cys Phe Thr Ser Pro Cys Val Ser Arg Val  
 595 600 605  
 Ile Gln Val Glu Pro Gln Ala Tyr Thr Glu Pro His Ser Asn Thr Arg  
 610 615 620  
 Tyr Ser Pro Pro Pro Pro Tyr Thr Ser His Ser Phe Ala His Glu Thr  
 625 630 635 640  
 His Ile Thr Met Gln Ser Thr Val Gln Leu Arg Thr Glu Tyr Asp Pro  
 645 650 655  
 His Thr His Val Tyr Tyr Thr Thr Ala Glu Pro Arg Ser Glu Ile Ser  
 660 665 670  
 Val Gln Pro Val Thr Val Thr Gln Asp Asn Leu Ser Cys Gln Ser Pro  
 675 680 685  
 Glu Ser Thr Ser Ser Thr Arg Asp Leu Leu Ser Gln Phe Ser Asp Ser  
 690 695 700

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Ser Leu His Cys Leu Glu Pro Pro Cys Thr Lys Trp Thr Leu Ser Ser  
 705 710 715 720  
 Phe Ala Glu Lys His Tyr Ala Pro Phe Leu Leu Lys Pro Lys Ala Lys  
 725 730 735  
 Val Val Val Ile Leu Leu Phe Leu Gly Leu Leu Gly Val Ser Leu Tyr  
 740 745 750  
 Gly Thr Thr Arg Val Arg Asp Gly Leu Asp Leu Thr Asp Ile Val Pro  
 755 760 765  
 Arg Glu Thr Arg Glu Tyr Asp Phe Ile Ala Ala Gln Phe Lys Tyr Phe  
 770 775 780  
 Ser Phe Tyr Asn Met Tyr Ile Val Thr Gln Lys Ala Asp Tyr Pro Asn  
 785 790 795 800  
 Ile Gln His Leu Leu Tyr Asp Leu His Lys Ser Phe Ser Asn Val Lys  
 805 810 815  
 Tyr Val Met Leu Glu Glu Asn Lys Gln Leu Pro Gln Met Trp Leu His  
 820 825 830  
 Tyr Phe Arg Asp Trp Leu Gln Gly Leu Gln Asp Ala Phe Asp Ser Asp  
 835 840 845  
 Trp Glu Thr Gly Arg Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp  
 850 855 860  
 Asp Gly Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp  
 865 870 875 880  
 Lys Pro Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala  
 885 890 895  
 Asp Gly Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp  
 900 905 910  
 Val Ser Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg  
 915 920 925  
 Pro His Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu  
 930 935 940  
 Thr Arg Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe  
 945 950 955 960  
 Pro Phe Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala  
 965 970 975  
 Ile Glu Lys Val Arg Val Ile Cys Asn Asn Tyr Thr Ser Leu Gly Leu  
 980 985 990  
 Ser Ser Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile  
 995 1000 1005  
 Ser Leu Arg His Trp Leu Leu Leu Ser Ile Ser Val Val Leu Ala Cys  
 1010 1015 1020  
 Thr Phe Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly  
 1025 1030 1035 1040

08916140-082197

Ile Ile Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met  
 1045 1050 1055  
 Met Gly Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu  
 1060 1065 1070  
 Ile Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu  
 1075 1080 1085  
 Ala Phe Leu Thr Ala Ile Gly Asp Lys Asn His Arg Ala Met Leu Ala  
 1090 1095 1100  
 Leu Glu His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu  
 1105 1110 1115 1120  
 Leu Gly Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg  
 1125 1130 1135  
 Tyr Phe Phe Ala Val Leu Ala Ile Leu Thr Val Leu Gly Val Leu Asn  
 1140 1145 1150  
 Gly Leu Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Cys Pro  
 1155 1160 1165  
 Glu Val Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro  
 1170 1175 1180  
 Glu Pro Pro Pro Ser Val Val Arg Phe Ala Val Pro Pro Gly His Thr  
 1185 1190 1195 1200  
 Asn Asn Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr  
 1205 1210 1215  
 Val Ser Gly Ile Ser Glu Glu Leu Arg Gln Tyr Glu Ala Gln Gln Gly  
 1220 1225 1230  
 Ala Gly Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro  
 1235 1240 1245  
 Val Phe Ala Arg Ser Thr Val Val His Pro Asp Ser Arg His Gln Pro  
 1250 1255 1260  
 Pro Leu Thr Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Ser  
 1265 1270 1275 1280  
 Pro Gly Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly  
 1285 1290 1295  
 Leu Arg Pro Pro Pro Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile Ser  
 1300 1305 1310  
 Thr Glu Gly His Ser Gly Pro Ser Asn Arg Asp Arg Ser Gly Pro Arg  
 1315 1320 1325  
 Gly Ala Arg Ser His Asn Pro Arg Asn Pro Thr Ser Thr Ala Met Gly  
 1330 1335 1340  
 Ser Ser Val Pro Ser Tyr Cys Gln Pro Ile Thr Thr Val Thr Ala Ser  
 1345 1350 1355 1360  
 Ala Ser Val Thr Val Ala Val His Pro Pro Pro Gly Pro Gly Arg Asn  
 1365 1370 1375

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(2) INFORMATION FOR SEQ ID NO:11:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

(2) INFORMATION FOR SEQ ID NO:12:

(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

(2) INFORMATION FOR SEQ ID NO:13:

SEQUENCE CHARACTERISTICS

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Phe Phe Trp Glu Gln Tyr

1

5

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGACGAATTC AARGTNCAYC ARYTNTGG

28

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGACGAATTC CYTCCCARAA RCANTC

26

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGACGAATTC YTNGANTGYT TYTGGA

27

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CATACCAGCC AAGCTTGTCN GGCCARTGCA T

31

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5288 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCCGGG GACCGCAAGG AGTGCCGCGG AAGCGCCCGA AGGACAGGCT CGCTCGGCGC	60
GCCGGCTCTC GCTCTTCCGC GAACTGGATG TGGGCAGCGG CGGCCGAGA GACCTCGGGA	120
CCCCCGCGCA ATGTGGCAAT GGAAGGCGCA GGGTCTGACT CCCCAGCAGC GGCCGCGGCC	180
GCAGCGGCAG CAGCGCCCGC CGTGTGAGCA GCAGCAGCGG CTGGTCTGTC AACCGGAGCC	240
CGAGCCCGAG CAGCCTGCGG CCAGCAGCGT CCTCGCAAGC CGAGCGCCCA GGCGCGCCAG	300
GAGCCCGCAG CAGCGGCAGC AGCGCGCCGG GCCGCCCGG AAGCCTCCGT CCCCAGCGCG	360
GCGGCGGCGG CGGCGGCGGC AACATGGCCT CGGCTGGTAA CGCCGCCGAG CCCCAGGACC	420
GCGGCGGCGG CGGCAGCGGC TGTATCGGTG CCCCAGGACG GCCGGCTGGA GGCGGGAGGC	480
GCAGACGGAC GGGGGGGCTG CGCCGTGCTG CCGCGCCGGA CCGGGACTAT CTGCACCGGC	540
CCAGCTACTG CGACGCCGCC TTCGCTCTGG AGCAGATTTC CAAGGGGAAG GCTACTGGCC	600
GGAAAGCGCC ACTGTGGCTG AGAGCGAAGT TTCAGAGACT CTTATTTAAA CTGGGTGTGT	660
ACATTCAAAA AAAGTGCAGC AAGTTCTTGG TTGTGGGCTT CCTCATATTT GGGGCCTTCG	720
CGGTGGGATT AAAAGCAGCG AACCTCGAGA CCAACGTGGA GGAGCTGTGG GTGGAAGTTG	780
GAGGACGAGT AAGTCGTGAA TTAAATTATA CTCGCCAGAA GATTGGAGAA GAGGCTATGT	840
TTAATCCTCA ACTCATGATA CAGACCCCTA AAGAAGAAGG TGCTAATGTC CTGACCACAG	900
AAGCGCTCCT ACAACACCTG GACTCGGCAC TCCAGGCCAG CCGTGTCCAT GTATACATGT	960
ACAACAGGCA GTGGAAATTG GAACATTTGT GTTACAAATC AGGAGAGCTT ATCACAGAAA	1020
CAGGTTACAT GGATCAGATA ATAGAATATC TTTACCCTTG TTTGATTATT ACACCTTTGG	1080
ACTGCTTCTG GGAAGGGGCG AAATTACAGT CTGGGACAGC ATACCTCCTA GGTAAACCTC	1140

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CTTTGCGGTG GACAAACTTC GACCCTTTGG AATTCCTGGA AGAGTTAAAG AAAATAAACT 1200  
 ATCAAGTGGA CAGCTGGGAG GAAATGCTGA ATAAGGCTGA GGTGGTGCAT GGTTACATGG 1260  
 ACCGCCCCTG CCTCAATCCG GCCGATCCAG ACTGCCCCGC CACAGCCCCC AACAAAAATT 1320  
 CAACCAAACC TCTTGATATG GCCCTTGTTT TGAATGGTGG ATGTCATGGC TTATCCAGAA 1380  
 AGTATATGCA CTGGCAGGAG GAGTTGATTG TGGGTGGCAC AGTCAAGAAC AGCACTGGAA 1440  
 AACTCGTCAG CGCCCATGCC CTGCAGACCA TGTTCCAGTT AATGACTCCC AAGCAAATGT 1500  
 ACGAGCACTT CAAGGGGTAC GAGTATGTCT CACACATCAA CTGGAACGAG GACAAAGCGG 1560  
 CAGCCATCCT GGAGGCCTGG CAGAGGACAT ATGTGGAGGT GGTTCATCAG AGTGTGCGAC 1620  
 AGAACTCCAC TCAAAAGGTG CTTTCCTTCA CCACCACGAC CCTGGACGAC ATCCTGAAAT 1680  
 CCTTCTCTGA CGTCAGTGTC ATCCGCGTGG CCAGCGGCTA CTTACTCATG CTCGCCTATG 1740  
 CCTGTCTAAC CATGCTGCGC TGGGACTGCT CCAAGTCCCA GGGTGCCGTG GGGCTGGCTG 1800  
 GCGTCCTGCT GGTGCACTG TCAGTGGCTG CAGGACTGGG CCTGTGCTCA TTGATCGGAA 1860  
 TTTCCCTTAA CGCTGCAACA ACTCAGGTTT TGCCATTTCT CGCTCTGGT GTTGGTGTGG 1920  
 ATGATGTTTT TCTTCTGGCC CACGCCTTCA GTGAAACAGG ACAGAATAAA AGAATCCCTT 1980  
 TTGAGGACAG GACCGGGGAG TGCCTGAAGC GCACAGGAGC CAGCGTGGCC CTCACGTCCA 2040  
 TCAGCAATGT CACAGCCTTC TTCATGGCCG CGTTAATCCC AATTCCCGCT CTGCGGGCGT 2100  
 TCTCCCTCCA GGCAGCGGTA GTAGTGGTGT TCAATTTTGC CATGGTTCTG CTCATTTTTC 2160  
 CTGCAATTCT CAGCATGGAT TTATATCGAC GCGAGGACAG GAGACTGGAT ATTTTCTGCT 2220  
 GTTTTACAAG CCCCTGCGTC AGCAGAGTGA TTCAGGTGA ACCTCAGGCC TACACCGACA 2280  
 CACACGACAA TACCCGCTAC AGCCCCCAC CTCCCTACAG CAGCCACAGC TTTGCCCATG 2340  
 AAACGCAGAT TACCATGCAG TCCACTGTCC AGCTCCGCAC GGAGTACGAC CCCCACACGC 2400  
 ACGTGTAATA CACCACCGCT GAGCCGCGCT CCGAGATCTC TGTGCAGCCC GTCACCGTGA 2460  
 CACAGGACAC CCTCAGCTGC CAGAGCCCAG AGAGCACCAG CTCCACAAGG GACCTGCTCT 2520  
 CCCAGTTCTC CGACTCCAGC CTCCACTGCC TCGAGCCCCC CTGTACGAAG TGGACACTCT 2580  
 CATCTTTTGC TGAGAAGCAC TATGCTCCTT TCCTCTTGAA ACCAAAAGCC AAGGTAGTGG 2640  
 TGATCTTCCT TTTTCTGGGC TTGCTGGGGG TCAGCCTTTA TGGCACCACC CGAGTGAGAG 2700  
 ACGGGCTGGA CCTTACGGAC ATTGTACCTC GGGAAACCAG AGAATATGAC TTTATTGCTG 2760  
 CACAATTCAA ATACTTTTCT TTCTACAACA TGTATATAGT CACCCAGAAA GCAGACTACC 2820  
 CGAATATCCA GCACTTACTT TACGACCTAC ACAGGAGTTT CAGTAACGTG AAGTATGTCA 2880  
 TGTGGAAGA AAACAAACAG CTTCCCAAAA TGTGGCTGCA CTAATTCAGA GACTGGCTTC 2940  
 AGTCACTTCA GGATGCATTT GACAGTGAAT GGGAAACCGG GAAAATCATG CCAACAATT 3000  
 ACAAGAATGG ATCAGACGAT GGAGTCCTTG CCTACAACT CCTGGTGCAA ACCGGCAGCC 3060

00916140-003197

GCGATAAGCC CATCGACATC AGCCAGTTGA CTAACAGCG TCTGGTGGAT GCAGATGGCA 3120  
 TCATTAATCC CAGCGCTTTC TACATCTACC TGACGGCTTG GGTCAGCAAC GACCCCGTCG 3180  
 CGTATGCTGC CTCCCAGGCC AACATCCGGC CACACCGACC AGAATGGGTC CACGACAAAG 3240  
 CCGACTACAT GCCTGAAACA AGGCTGAGAA TCCCGGCAGC AGAGCCCATC GAGTATGCCC 3300  
 AGTTCCCTTT CTACCTCAAC GGGTTGCGGG ACACCTCAGA CTTTGTGGAG GCAATTGAAA 3360  
 AAGTAAGGAC CATCTGCAGC AACTATACGA GCCTGGGGCT GTCCAGTTAC CCCAACGGCT 3420  
 ACCCTTCCT CTTCTGGGAG CAGTACATCG GCCTCCGCCA CTGGCTGCTG CTGTTTCATCA 3480  
 GCGTGGTGTT GGCCTGCACA TTCCTCGTGT GCGCTGTCTT CTTTCTGAAC CCCTGGACGG 3540  
 CCGGGATCAT TGTGATGGTC CTGGCGCTGA TGACGGTCGA GCTGTTCCGC ATGATGGGCC 3600  
 TCATCGGAAT CAAGCTCAGT GCCGTGCCCC TGGTCATCCT GATCGCTTCT GTTGGCATAG 3660  
 GAGTGGAGTT CACCGTTCAC GTTGCTTTGG CTTTCTGAC GGCCATCGGC GACAAGAACC 3720  
 GCAGGGCTGT GCTTGCCCTG GAGCACATGT TTGCACCCGT CCTGGATGGC GCCGTGTCCA 3780  
 CTCTGCTGGG AGTGCTGATG CTGGCGGGAT CTGAGTTCGA CTTCAATTGC AGGTATTTCT 3840  
 TTGCTGTGCT GGCATCCTC ACCATCCTCG GCGTTCTCAA TGGGCTGGTT TTGCTTCCCG 3900  
 TGCTTTTGTC TTTCTTTGGA CCATATCCTG AGGTGTCTCC AGCCAACGGC TTGAACCGCC 3960  
 TGCCACACACC CTCCCCTGAG CCACCCCCCA GCGTGGTCCG CTTGCGCATG CCGCCCGGCC 4020  
 ACACGCACAG CGGGTCTGAT TCCTCCGACT CGGAGTATAG TTCCCAGACG ACAGTGTGAG 4080  
 GCCTCAGCGA GGAGCTTCGG CACTACGAGG CCCAGCAGGG CGCGGGAGGC CCTGCCCACC 4140  
 AAGTGATCGT GGAAGCCACA GAAAACCCCG TCTTCGCCCA CTCCACTGTG GTCCATCCCG 4200  
 AATCCAGGCA TCACCCACCC TCGAACCCGA GACAGCAGCC CCACCTGGAC TCAGGGTCCC 4260  
 TGCCCTCCCGG ACGGCAAGGC CAGCAGCCCC GCAGGGACCC CCCCAGAGAA GGCTTGTTGGC 4320  
 CACCCCTCTA CAGACCGCGC AGAGACGCTT TTGAAATTC TACTGAAGGG CATTCTGGCC 4380  
 CTAGCAATAG GGCCCGCTGG GGCCCTCGCG GGGCCCGTTC TCACAACCCT CGGAACCCAG 4440  
 CGTCCACTGC CATGGGCAGC TCCGTGCCCC GCTACTGCCA GCCCATCACC ACTGTGACGG 4500  
 CTTCTGCCTC CGTGA CTGTC GCCGTGCACC CGCCGCTGT CCCTGGGCCT GGGCGGAACC 4560  
 CCGAGGGGG ACTCTGCCCA GGCTACCCTG AGACTGACCA CGGCCTGTTT GAGGACCCCC 4620  
 ACGTGCCCTT CCACGTCCGG TGTGAGAGGA GGGATTGCAA GGTGGAAGTC ATTGAGCTGC 4680  
 AGGACGTGGA ATGCGAGGAG AGGCCCCGGG GAAGCAGCTC CAACTGAGGG TGATTAAAT 4740  
 CTGAAGCAAA GAGGCCAAAG ATTGGAACC CCCCACCCCC ACCTCTTTCC AGAACTGCTT 4800  
 GAAGAGAACT GGTGAGGTT ATGGAAAAGA TGCCCTGTGC CAGGACAGCA GTTCATTGTT 4860  
 ACTGTAACCG ATTGTATTAT TTTGTTAAAT ATTTCTATAA ATATTAAAGA GATGTACACA 4920

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TGTGTAATAT AGGAAGGAAG GATGTAAAGT GGTATGATCT GGGGCTTCTC CACTCCTGCC 4980  
 CCAGAGTGTG GAGGCCACAG TGGGGCCTCT CCGTATTTGT GCATTGGGCT CCGTGCCACA 5040  
 ACCAAGCTTC ATTAGTCTTA AATTCAGCA TATGTTGCTG CTGCTTAAAT ATTGTATAAT 5100  
 TTACTTGTAT AATTCTATGC AAATATTGCT TATGTAATAG GATTATTTTG TAAAGGTTTC 5160  
 TGTTTAAAT ATTTTAAATT TGCATATCAC AACCTGTGG TAGTATGAAA TGTTACTGTT 5220  
 AACTTTCAAA CACGCTATGC GTGATAATTT TTTTGTTTAA TGAGCAGATA TGAAGAAAGC 5280  
 CCGGAATT 5288

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Ser Ala Gly Asn Ala Ala Glu Pro Gln Asp Arg Gly Gly Gly  
 1 5 10 15  
 Gly Ser Gly Cys Ile Gly Ala Pro Gly Arg Pro Ala Gly Gly Gly Arg  
 20 25 30  
 Arg Arg Arg Thr Gly Gly Leu Arg Arg Ala Ala Ala Pro Asp Arg Asp  
 35 40 45  
 Tyr Leu His Arg Pro Ser Tyr Cys Asp Ala Ala Phe Ala Leu Glu Gln  
 50 55 60  
 Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp Leu Arg  
 65 70 75 80  
 Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile Gln Lys  
 85 90 95  
 Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly Ala Phe  
 100 105 110  
 Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu Glu Leu  
 115 120 125  
 Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr Thr Arg  
 130 135 140  
 Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met Ile Gln  
 145 150 155 160  
 Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala Leu Leu  
 165 170 175  
 Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val Tyr Met

0091640-083197

180					185					190					
Tyr	Asn	Arg	Gln	Trp	Lys	Leu	Glu	His	Leu	Cys	Tyr	Lys	Ser	Gly	Glu
		195					200					205			
Leu	Ile	Thr	Glu	Thr	Gly	Tyr	Met	Asp	Gln	Ile	Ile	Glu	Tyr	Leu	Tyr
	210					215					220				
Pro	Cys	Leu	Ile	Ile	Thr	Pro	Leu	Asp	Cys	Phe	Trp	Glu	Gly	Ala	Lys
225					230					235					240
Leu	Gln	Ser	Gly	Thr	Ala	Tyr	Leu	Leu	Gly	Lys	Pro	Pro	Leu	Arg	Trp
				245					250					255	
Thr	Asn	Phe	Asp	Pro	Leu	Glu	Phe	Leu	Glu	Glu	Leu	Lys	Lys	Ile	Asn
			260					265					270		
Tyr	Gln	Val	Asp	Ser	Trp	Glu	Glu	Met	Leu	Asn	Lys	Ala	Glu	Val	Gly
		275					280					285			
His	Gly	Tyr	Met	Asp	Arg	Pro	Cys	Leu	Asn	Pro	Ala	Asp	Pro	Asp	Cys
	290					295					300				
Pro	Ala	Thr	Ala	Pro	Asn	Lys	Asn	Ser	Thr	Lys	Pro	Leu	Asp	Met	Ala
305					310					315					320
Leu	Val	Leu	Asn	Gly	Gly	Cys	His	Gly	Leu	Ser	Arg	Lys	Tyr	Met	His
				325					330					335	
Trp	Gln	Glu	Glu	Leu	Ile	Val	Gly	Gly	Thr	Val	Lys	Asn	Ser	Thr	Gly
			340					345						350	
Lys	Leu	Val	Ser	Ala	His	Ala	Leu	Gln	Thr	Met	Phe	Gln	Leu	Met	Thr
		355					360					365			
Pro	Lys	Gln	Met	Tyr	Glu	His	Phe	Lys	Gly	Tyr	Glu	Tyr	Val	Ser	His
	370					375					380				
Ile	Asn	Trp	Asn	Glu	Asp	Lys	Ala	Ala	Ala	Ile	Leu	Glu	Ala	Trp	Gln
385					390					395					400
Arg	Thr	Tyr	Val	Glu	Val	Val	His	Gln	Ser	Val	Ala	Gln	Asn	Ser	Thr
				405					410					415	
Gln	Lys	Val	Leu	Ser	Phe	Thr	Thr	Thr	Thr	Leu	Asp	Asp	Ile	Leu	Lys
			420					425					430		
Ser	Phe	Ser	Asp	Val	Ser	Val	Ile	Arg	Val	Ala	Ser	Gly	Tyr	Leu	Leu
		435					440					445			
Met	Leu	Ala	Tyr	Ala	Cys	Leu	Thr	Met	Leu	Arg	Trp	Asp	Cys	Ser	Lys
	450					455					460				
Ser	Gln	Gly	Ala	Val	Gly	Leu	Ala	Gly	Val	Leu	Leu	Val	Ala	Leu	Ser
465					470					475					480
Val	Ala	Ala	Gly	Leu	Gly	Leu	Cys	Ser	Leu	Ile	Gly	Ile	Ser	Phe	Asn
				485					490					495	
Ala	Ala	Thr	Thr	Gln	Val	Leu	Pro	Phe	Leu	Ala	Leu	Gly	Val	Gly	Val
				500				505					510		
Asp	Asp	Val	Phe	Leu	Leu	Ala	His	Ala	Phe	Ser	Glu				

515					520					525					
Lys	Arg	Ile	Pro	Phe	Glu	Asp	Arg	Thr	Gly	Glu	Cys	Leu	Lys	Arg	Thr
530						535					540				
Gly	Ala	Ser	Val	Ala	Leu	Thr	Ser	Ile	Ser	Asn	Val	Thr	Ala	Phe	Phe
545					550					555					560
Met	Ala	Ala	Leu	Ile	Pro	Ile	Pro	Ala	Leu	Arg	Ala	Phe	Ser	Leu	Gln
				565					570					575	
Ala	Ala	Val	Val	Val	Val	Phe	Asn	Phe	Ala	Met	Val	Leu	Leu	Ile	Phe
				580				585						590	
Pro	Ala	Ile	Leu	Ser	Met	Asp	Leu	Tyr	Arg	Arg	Glu	Asp	Arg	Arg	Leu
		595					600					605			
Asp	Ile	Phe	Cys	Cys	Phe	Thr	Ser	Pro	Cys	Val	Ser	Arg	Val	Ile	Gln
610						615					620				
Val	Glu	Pro	Gln	Ala	Tyr	Thr	Asp	Thr	His	Asp	Asn	Thr	Arg	Tyr	Ser
625					630					635					640
Pro	Pro	Pro	Pro	Tyr	Ser	Ser	His	Ser	Phe	Ala	His	Glu	Thr	Gln	Ile
				645					650					655	
Thr	Met	Gln	Ser	Thr	Val	Gln	Leu	Arg	Thr	Glu	Tyr	Asp	Pro	His	Thr
			660					665					670		
His	Val	Tyr	Tyr	Thr	Thr	Ala	Glu	Pro	Arg	Ser	Glu	Ile	Ser	Val	Gln
		675					680					685			
Pro	Val	Thr	Val	Thr	Gln	Asp	Thr	Leu	Ser	Cys	Gln	Ser	Pro	Glu	Ser
	690					695					700				
Thr	Ser	Ser	Thr	Arg	Asp	Leu	Leu	Ser	Gln	Phe	Ser	Asp	Ser	Ser	Leu
705					710					715					720
His	Cys	Leu	Glu	Pro	Pro	Cys	Thr	Lys	Trp	Thr	Leu	Ser	Ser	Phe	Ala
				725					730					735	
Glu	Lys	His	Tyr	Ala	Pro	Phe	Leu	Leu	Lys	Pro	Lys	Ala	Lys	Val	Val
			740					745					750		
Val	Ile	Phe	Leu	Phe	Leu	Gly	Leu	Leu	Gly	Val	Ser	Leu	Tyr	Gly	Thr
		755					760					765			
Thr	Arg	Val	Arg	Asp	Gly	Leu	Asp	Leu	Thr	Asp	Ile	Val	Pro	Arg	Glu
	770					775					780				
Thr	Arg	Glu	Tyr	Asp	Phe	Ile	Ala	Ala	Gln	Phe	Lys	Tyr	Phe	Ser	Phe
785				790						795					800
Tyr	Asn	Met	Tyr	Ile	Val	Thr	Gln	Lys	Ala	Asp	Tyr	Pro	Asn	Ile	Gln
				805					810					815	
His	Leu	Leu	Tyr	Asp	Leu	His	Arg	Ser	Phe	Ser	Asn	Val	Lys	Tyr	Val
			820					825					830		
Met	Leu	Glu	Glu	Asn	Lys	Gln	Leu	Pro	Lys	Met	Trp	Leu	His	Tyr	Phe
		835					840					845			
Arg	Asp	Trp	Leu	Gln	Gly	Leu	Gln	Asp	Ala	Phe	Asp	Ser	Asp	Trp	Glu
	850						855				860				

00916140-082197



Thr Gly Lys Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp Asp Gly  
 865 870 875 880  
 Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp Lys Pro  
 885 890 895  
 Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala Asp Gly  
 900 905 910  
 Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp Val Ser  
 915 920 925  
 Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg Pro His  
 930 935 940  
 Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu Thr Arg  
 945 950 955 960  
 Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe Pro Phe  
 965 970 975  
 Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala Ile Glu  
 980 985 990  
 Lys Val Arg Thr Ile Cys Ser Asn Tyr Thr Ser Leu Gly Leu Ser Ser  
 995 1000 1005  
 Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile Gly Leu  
 1010 1015 1020  
 Arg His Trp Leu Leu Leu Phe Ile Ser Val Val Leu Ala Cys Thr Phe  
 1025 1030 1035 1040  
 Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly Ile Ile  
 1045 1050 1055  
 Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met Met Gly  
 1060 1065 1070  
 Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu Ile Ala  
 1075 1080 1085  
 Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu Ala Phe  
 1090 1095 1100  
 Leu Thr Ala Ile Gly Asp Lys Asn Arg Arg Ala Val Leu Ala Leu Glu  
 1105 1110 1115 1120  
 His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu Leu Gly  
 1125 1130 1135  
 Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg Tyr Phe  
 1140 1145 1150  
 Phe Ala Val Leu Ala Ile Leu Thr Ile Leu Gly Val Leu Asn Gly Leu  
 1155 1160 1165  
 Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Tyr Pro Glu Val  
 1170 1175 1180  
 Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro Glu Pro  
 1185 1190 1195 1200

08916140-082197

Pro Pro Ser Val Val Arg Phe Ala Met Pro Pro Gly His Thr His Ser  
 1205 1210 1215  
 Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr Val Ser  
 1220 1225 1230  
 Gly Leu Ser Glu Glu Leu Arg His Tyr Glu Ala Gln Gln Gly Ala Gly  
 1235 1240 1245  
 Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro Val Phe  
 1250 1255 1260  
 Ala His Ser Thr Val Val His Pro Glu Ser Arg His His Pro Pro Ser  
 1265 1270 1275 1280  
 Asn Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Pro Pro Gly  
 1285 1290 1295  
 Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly Leu Trp  
 1300 1305 1310  
 Pro Pro Leu Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile Ser Thr Glu  
 1315 1320 1325  
 Gly His Ser Gly Pro Ser Asn Arg Ala Arg Trp Gly Pro Arg Gly Ala  
 1330 1335 1340  
 Arg Ser His Asn Pro Arg Asn Pro Ala Ser Thr Ala Met Gly Ser Ser  
 1345 1350 1355 1360  
 Val Pro Gly Tyr Cys Gln Pro Ile Thr Thr Val Thr Ala Ser Ala Ser  
 1365 1370 1375  
 Val Thr Val Ala Val His Pro Pro Pro Val Pro Gly Pro Gly Arg Asn  
 1380 1385 1390  
 Pro Arg Gly Gly Leu Cys Pro Gly Tyr Pro Glu Thr Asp His Gly Leu  
 1395 1400 1405  
 Phe Glu Asp Pro His Val Pro Phe His Val Arg Cys Glu Arg Arg Asp  
 1410 1415 1420  
 Ser Lys Val Glu Val Ile Glu Leu Gln Asp Val Glu Cys Glu Glu Arg  
 1425 1430 1435 1440  
 Pro Arg Gly Ser Ser Ser Asn  
 1445

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